

SYSTEMATIC REVIEW AND META-ANALYSIS

Warfarin dosing algorithms: A systematic review

Innocent G. Asiiimwe¹  | Eunice J. Zhang¹ | Rostam Osanlou¹ |
Andrea L. Jorgensen² | Munir Pirmohamed¹ 

¹The Wolfson Centre for Personalized Medicine, MRC Centre for Drug Safety Science, Department of Pharmacology and Therapeutics, Institute of Systems, Molecular and Integrative Biology, University of Liverpool, United Kingdom

²Department of Biostatistics, Institute of Population Health Sciences, University of Liverpool, United Kingdom

Correspondence

Innocent G. Asiiimwe and Professor Sir Munir Pirmohamed, The Wolfson Centre for Personalised Medicine, Block A Waterhouse Buildings, 1–5 Brownlow Street, Liverpool, L69 3GL.

Email: i.asiiimwe@liverpool.ac.uk;
munirp@liverpool.ac.uk

Funding information

National Institute for Health Research, Grant/Award Number: 16/137/101

Aims: Numerous algorithms have been developed to guide warfarin dosing and improve clinical outcomes. We reviewed the algorithms available for various populations and the covariates, performances and risk of bias of these algorithms.

Methods: We systematically searched MEDLINE up to 20 May 2020 and selected studies describing the development, external validation or clinical utility of a multivariable warfarin dosing algorithm. Two investigators conducted data extraction and quality assessment.

Results: Of 10 035 screened records, 266 articles were included in the review, describing the development of 433 dosing algorithms, 481 external validations and 52 clinical utility assessments. Most developed algorithms were for dose initiation (86%), developed by multiple linear regression (65%) and mostly applicable to Asians (49%) or Whites (43%). The most common demographic/clinical/environmental covariates were age (included in 401 algorithms), concomitant medications (270 algorithms) and weight (229 algorithms) while CYP2C9 (329 algorithms), VKORC1 (319 algorithms) and CYP4F2 (92 algorithms) variants were the most common genetic covariates. Only 26% and 7% algorithms were externally validated and evaluated for clinical utility, respectively, with <2% of algorithm developments and external validations being rated as having a low risk of bias.

Conclusion: Most warfarin dosing algorithms have been developed in Asians and Whites and may not be applicable to under-served populations. Few algorithms have been externally validated, assessed for clinical utility, and/or have a low risk of bias which makes them unreliable for clinical use. Algorithm development and assessment should follow current methodological recommendations to improve reliability and applicability, and under-represented populations should be prioritized.

KEYWORDS

clinical factors, demographic factors, dosing algorithms, genetic factors, warfarin

Andrea L. Jorgensen and Munir Pirmohamed contributed equally

[Correction added on 2 December 2020, after first online publication: Table 1 has been corrected in this current version.]

This is an open access article under the terms of the Creative Commons Attribution License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2020 The Authors. British Journal of Clinical Pharmacology published by John Wiley & Sons Ltd on behalf of British Pharmacological Society

1 | INTRODUCTION

Warfarin remains the most commonly prescribed oral anticoagulant for the management of thromboembolic disorders.¹ However, dosing remains challenging due to warfarin's narrow therapeutic index and highly variable clinical response. These dosing challenges usually result in a high frequency of adverse effects (thrombosis and bleeding) as well as an increased burden to the patient (e.g. more frequent monitoring), which could impact quality of life and lead to treatment discontinuation of an otherwise highly efficacious drug.² To better predict an individual's warfarin dose requirements, numerous dose-prediction algorithms based on demographic, clinical, environment and genetic factors have been developed.^{3,4} Algorithms incorporating only demographic, clinical and environmental factors have been designated as *clinical* and those additionally incorporating genetic factors as *pharmacogenetic*.⁵

The availability of numerous published dosing algorithms provides a wealth of information but makes navigating the literature to identify which algorithms to use or recommend, and in which patients/populations difficult. This task becomes more complicated if it is not clear if the identified algorithms have low risks of bias, have been externally validated and/or have been evaluated for clinical utility. The Clinical Pharmacogenetics Implementation Consortium (CPIC) has recommended the use of 4 dosing algorithms.¹ However, these may not be applicable to non-Caucasians or for some categories of patients such as those with international normalized ratio (INR) targets outside of the 2–3 range.^{1,6,7}

Previous reviews have attempted to describe available dosing algorithms but most, if not all, have had the main limitation of focusing on a limited number of algorithms. For example Saffian *et al.*⁸ evaluated 16 algorithms but these were only from studies that had: (i) evaluated the algorithm's predictive ability in the form of a high resolution scatterplot (observed vs predicted maintenance doses); (ii) used a validation dataset; and (iii) included at least 5 patients requiring warfarin at a dose >7 mg/d. Other reviews including those by Verhoef *et al.*⁹ (32 algorithms) and Shendre *et al.*¹⁰ (50 eligible studies) have been narrative in nature and consequently neither reported a detailed search strategy nor assessed the risk of bias of included studies. Additionally, both these narrative reviews included only pharmacogenetic algorithms and the Shendre *et al.*¹⁰ review additionally excluded studies that did not involve European or African ancestry populations. To methodologically assess and describe the knowledge base accumulated so far, we have undertaken this systematic review, which includes both clinical and pharmacogenetic algorithms with no population-based exclusion criteria. Our aim was to accurately and comprehensively summarize which algorithms are available for which populations and the covariates (demographic, clinical, environmental, genetic), performances and the risk of bias of these algorithms.

2 | METHODS

2.1 | Search strategy and selection criteria

A predefined protocol (PROSPERO: CRD42019147995), based on the principles set in the CHARMS (CHecklist for critical Appraisal and data extraction for systematic Reviews of prediction Modelling Studies) checklist,¹¹ and PROBAST (Prediction model Risk Of Bias Assessment Tool), a tool meant to assess the risk of bias and applicability of prediction model studies¹² was followed. This report adheres to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) statement (Table S1). MEDLINE records (from 1946 to 22 August 2019) were searched using medical subject headings (MeSH terms) and text words related to “warfarin”, “algorithm” and “dosing” (Table S2). A second MEDLINE search was conducted on 20 May 2020 to identify records published after our first search. Lists of references from the identified studies were hand-searched to identify further eligible studies. Non-English language studies were excluded.

Observational (e.g. cohort studies) and interventional (e.g. randomised controlled trials) studies that developed, validated or assessed the impact/clinical utility of warfarin dosing algorithms in any warfarin-treated population were included. For development studies, those that modelled at least 2 predictor variables (not counting dose and INR readings for dose-revision algorithms) and either: (i) explicitly stated in their aims that they were developing a dosing algorithm; or (ii) reported dosing equations, nomograms, charts, tables, computer programs etc. that can be used to provide a daily or weekly dose, were included. In all cases, the included predictors had to have been reported. Unless enough details pertaining to algorithm development were available in an external validation or clinical utility assessment study or elsewhere (corresponding development study, other studies), external validation or clinical utility assessment studies were excluded. Additionally, for a clinical utility assessment study to be included, a comparison between a dosing algorithm with an alternative strategy (such as existing clinical practice) was a prerequisite. For the purposes of this review, clinical utility¹³ was defined as the demonstration that a dosing algorithm improved the quality of anticoagulation (based on the time spent in the therapeutic INR range) or lead to better clinical endpoints (such as fewer bleeding episodes). Not to be confused with the outcome to be predicted in the individual studies (i.e. the stable warfarin dose), the primary outcome of interest in this review was the warfarin dose-prediction algorithm developed, and whether it was externally validated or evaluated for clinical utility in the included studies.

2.2 | Data extraction and quality assessment

One reviewer (I.G.A.) screened titles and abstracts of the retrieved bibliographic records for eligibility. For all stages, a second reviewer (R.O.) independently checked a random 10% of the records to check for consistency. Disagreements were resolved by consensus and because the first reviewer was consistent with regard to following agreed upon criteria, only the first reviewer continued reviewing the

remaining records. A data extraction form was adapted from the CHARMS¹¹ and PROBAST¹² tools, piloted in a subset of randomly selected included papers and used to extract relevant information related to participants, predictors, outcome, analysis and results. When a single publication reported both development and external validation studies (and/or clinical utility assessments), or multiple algorithms, each study/algorithm was assessed separately.¹² The exception was studies that reported the warfarindosing.com platform—although this platform incorporates multiple algorithms, it was not possible to separate the individual algorithms and so it was considered as 2, the clinical and pharmacogenetic Gage algorithms.¹⁴ Algorithm updating/extension studies in which new predictors were added to existing algorithms were considered as new algorithm development studies.¹²

To assess the methodological quality of each included development or external validation study, the 2 reviewers used the PROBAST tool.¹² Although this tool focuses on prediction models that consider binary or time-to-event outcomes and studies that use generalized linear modelling, its authors encourage its use in studies that consider other outcomes and other machine learning techniques such as those explored in this review.¹² It should, however, be tailored to these other outcomes/techniques as we did in Tables S3 and S4 and Figure S1. For reasons detailed in Table S3, emphasis was placed on the assessment of the risk of bias in the analysis domain. We did not assess the methodological quality (and performance) of clinical utility

(impact) assessment studies since these have been previously explored in several systematic reviews and meta-analyses.^{15–22}

2.3 | Data synthesis

This systematic review was qualitative in nature and no attempt to quantitatively synthesise studies by way of meta-analysis was conducted. Consequently, heterogeneity measures and publication bias were not explored. The descriptive results (i.e. proportions and measures of central tendency and dispersion) are presented in structured tables, graphically and as a narrative summary. Where appropriate, the results were stratified according to the type of algorithm (clinical vs pharmacogenetic) and ethnic populations for which they were developed. For the purposes of stratifying by population, we used the 4 categories (White, Asian, Black and Mixed/Other) reported by 1 of the largest warfarin-related studies to date, the International Warfarin Pharmacogenetics Consortium (IWPC) study.²³ Where these race categories were unreported, country was used as a proxy (for example populations from China were categorized as Asian while populations from northern Europe as White). Regarding which algorithm would be relevant to a given population, we arbitrarily chose a 5% cut-off, i.e. an algorithm that recruited at least 5% of a given population would be applicable to that population. These

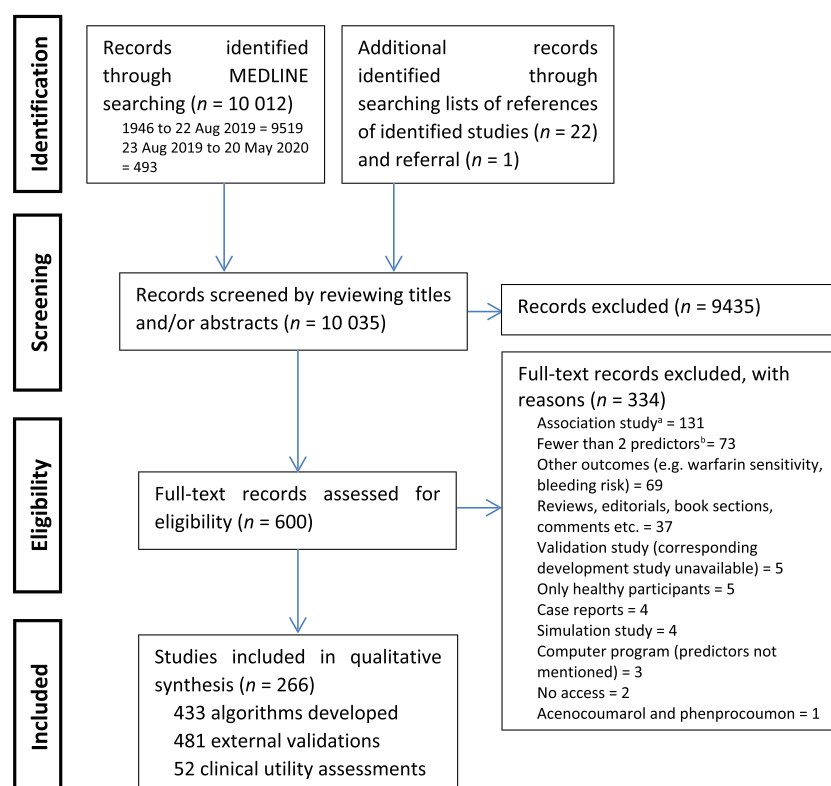


FIGURE 1 PRISMA flow chart of included studies. ^aIncludes studies that neither stated in their aims that they were developing/validating a dosing algorithm nor reported dosing equations, nomograms, charts, tables, or other tools that can be used to provide a daily or weekly dose.

^bPrior doses and international normalized ratios not counted

descriptive analyses were conducted in R (version 3.6.1).²⁴ No sensitivity analyses were conducted.

2.4 | Nomenclature of targets and ligands

Key protein targets and ligands in this article are hyperlinked to corresponding entries in <http://www.guidetopharmacology.org>, the common portal for data from the IUPHAR/BPS Guide to PHARMACOLOGY.

3 | RESULTS

We aimed to summarize which algorithms are available for which populations, and the covariates, performances and risk of bias of these algorithms. Figure 1 illustrates the literature search and selection process; 10 035 records were identified of which 9435 were excluded based on the title and abstract. Of 600 full text records assessed for eligibility, 266 met the eligibility criteria and were included in the qualitative synthesis. Of these, 205, 123 and 32 articles, respectively, described algorithm development, external validation and clinical utility assessment. Some articles described both algorithm development and external validation ($n = 74$), algorithm development and clinical utility assessment ($n = 10$), external validation and clinical utility assessment ($n = 15$) while 5 articles reported all 3 components (Figure S2). The included articles described the development of 433 dosing algorithms, 481 external validations and 52 clinical utility assessments, whose characteristics are summarised in Table 1 and detailed in Tables S5 and S6 (algorithm development), Table S7 (external validations), and Table S8 (clinical utility assessments).

Out of all date ranges investigated, the period during which most algorithm developments/evaluations were published was 2011–2015 in which 175 (41%), 224 (47%) and 18 (35%) algorithms were developed, externally validated and assessed for clinical utility, respectively (Table 1, Figure 2). The median sample sizes for these studies were 229 (range 18–10 673), 125 (28–2181) and 234 (10–2343), respectively. Children were studied less often—algorithm developments, external validations and clinical utility assessments in children were 11 (3%), 26 (5%) and 3 (6%), respectively. Asia had the highest number of algorithm developments ($n = 175$, 40%) and external validations ($n = 208$, 43%), while North America had the highest rate of clinical utility assessments ($n = 25$, 48%). Most of the developed algorithms included both clinical and genetic covariates ($n = 344$, 79%), were mostly for dose-initiation ($n = 373$, 86%), were developed using multiple linear regression ($n = 280$, 65%) and presented a regression formula that could be used to compute a weekly or daily dose ($n = 239$, 55%). Of the developed algorithms, 111 (26%) and 30 (7%) algorithms were respectively externally validated or assessed for clinical utility at least once (Table S9). The 5 most externally validated algorithms were all dose-initiation pharmacogenetic algorithms and included those by the IWPC²³ ($n = 72$ external validations), Gage¹⁴ ($n = 46$), Sconce²⁵ ($n = 32$), Wadelius²⁶ ($n = 20$) and Huang²⁷ ($n = 19$)

while the 4 most clinically assessed algorithms were the Gage pharmacogenetic algorithm¹⁴ ($n = 8$ clinical utility assessments), IWPC pharmacogenetic algorithm²³ ($n = 7$), Gage clinical algorithm¹⁴ ($n = 5$) and Lenzini dose revision pharmacogenetic algorithm²⁸ ($n = 4$). Consequently, most external validations were conducted on pharmacogenetic ($n = 432$ external validations, 90%) and dose initiation ($n = 443$, 92%) algorithms, algorithms developed using multiple linear regression ($n = 458$, 95%) and those that presented a regression formula ($n = 453$, 94%). A similar trend was observed for the clinical utility assessments (Table 1).

3.1 | Study populations

Of the 433 developed algorithms, 186 (43%), 210 (49%), 121 (28%) and 77 (18%) used datasets that included at least 5% White, 5% Asian, 5% Black and 5% Mixed/Other participants, respectively (Table 1). For the studies including at least 5% White participants, the median percentage of White participants was 90% (range 33–100%; Table S10). Corresponding values for Asian, Black and Mixed/Other cohorts were 100% (7–100%; Table S11), 14% (5–100%; Table S12) and 71% (5–100%; Table S13), respectively. Other characteristics stratified by populations are detailed in Tables S10–S13. For the developed algorithms that included at least 5% White participants in their datasets, 54 (29%) and 20 (11%) algorithms were respectively externally validated and assessed for clinical utility at least once (Table S14). The corresponding values were 55 (26%) and 10 (5%) for Asians (Table S15), 34 (28%) and 10 (8%) for Blacks (Table S16), and 14 (18%) and 2 (3%) for Mixed/Other (Table S16). It is important to note that these algorithms were not always validated in populations for whom they were developed.

3.2 | Predictors

During algorithm development, all 433 algorithms explored demographic, clinical, and environmental predictors and for these the median number of predictors included in the final algorithms was 5 (range 0–23). Conversely, only 346 algorithms explored genetic factors with the median number of genetic predictors included in the final algorithms being 3 (range 1–205). The predictors included in at least 10 algorithms are shown in Figure 3. Age (included in 401 algorithms), concomitant medications (270 algorithms, amiodarone in 201 algorithms), weight (229 algorithms) and sex (141 algorithms) were the 4 most common demographic/clinical/environmental predictors. Comorbidities were included in 100 algorithms and these included renal disease (42 algorithms), hepatic disease (40 algorithms), hypertension (27 algorithms) and diabetes mellitus (26 algorithms). The genes most frequently included in the pharmacogenetic algorithms were **CYP2C9** (329 algorithms), **VKORC1** (319 algorithms), **CYP4F2** (92 algorithms) and **APOE** (11 algorithms). **CYP2C9** variants included **CYP2C9*2** (in 206 algorithms), **CYP2C9*3** (316 algorithms) and other variants (64 algorithms), while **VKORC1** variants included

TABLE 1 Summary characteristics of algorithm developments, external validations, and clinical utility assessments

Characteristic	Algorithm development (n = 433)	External validations (n = 481)	Clinical utility assessments (n = 52)
Publication year, n (%)			
2000 and before	7 (1.6)	-	-
2001 to 2005	12 (2.8)	3 (0.6)	2 (3.8)
2006 to 2010	75 (17.3)	81 (16.8)	12 (23.1)
2011 to 2015	175 (40.4)	224 (46.6)	18 (34.6)
2016 to 2020	164 (37.9)	173 (36.0)	17 (32.7)
Sample size, median (range)	229 (18–10,673)	125 (28–2,181)	234 (10–2,343)
Participants (included), n (%)			
≥5% white	186 (43.0)	205 (42.6)	36 (69.2)
≥5% Asian	210 (48.5)	277 (57.6)	17 (32.7)
≥5% black	121 (27.9)	115 (23.9)	16 (30.8)
≥5% mixed/other	77 (17.8)	62 (12.9)	2 (3.8)
Adults	422 (97.5)	455 (94.6)	49 (94.2)
Children	11 (2.5)	26 (5.4)	3 (5.8)
Location, n (%)			
Africa ^a	2 (0.5)	2 (0.4)	-
Asia ^b	175 (40.4)	208 (43.2)	14 (26.9)
Europe	34 (7.9) 121	55 (11.4)	11 (21.2)
North America	136 (31.4)	121 (25.2)	25 (48.1)
South America	15 (3.5)	21 (4.4)	-
Middle East	30 (6.9)	25 (5.2)	2 (3.8)
Oceania	-	8 (1.7)	-
Multiple	41 (9.5)	41 (8.5)	-
Covariates included, n (%)			
Clinical ^c only	87 (20.1)	49 (10.2)	11 (21.2)
Genetic only ^d	2 (0.5)	-	-
Clinical ^c and genetic	344 (79.4)	432 (89.8)	41 (78.8)
Application time, n (%)			
Dose initiation	373 (86.1)	443 (92.1)	40 (76.9)
Dose revision	41 (9.5)	31 (6.4)	10 (19.2)
Both initiation and revision ^e	19 (4.4)	7 (1.5)	2 (3.8)
Modelling techniques, n (%)			
Artificial neural network	32 (7.4)	2 (0.4)	1 (1.9)
Multiple linear regression	280 (64.7)	458 (95.2)	47 (90.4)
Nonlinear mixed effects ^f	14 (3.2)	7 (1.5)	3 (5.8)
Support vector regression	27 (6.2)	2 (0.4)	-
Other ^g	66 (15.2)	9 (1.9)	-
Unclear	10 (2.3)	3 (0.6)	1 (1.9)
Algorithm presentation, n (%)			
Computer program ^h	10 (2.3)	4 (0.8)	4 (7.7)
Nomogram/table	9 (2.1)	3 (0.6)	-
Regression formula	239 (55.2)	453 (94.2)	47 (90.4)
None	175 (40.4)	21 (4.4)	1 (1.9)

^aExcludes Egypt, which is under Middle East.^bMostly China (131 algorithm developments, 120 external validations and 11 clinical utility assessments). This was followed by South Korea (16 algorithm developments, 59 external validations and 1 clinical utility assessment) and Japan (10 algorithm developments and 14 external validations).^cClinical includes clinical, demographic, and environmental variables.^dClinical factors also considered during the modelling.^eAll incorporate pharmacokinetic and/or pharmacodynamic techniques.^fUsed to fit pharmacokinetic/pharmacodynamic-based algorithms.^gSee Table S6 for details.^hOr online tool.

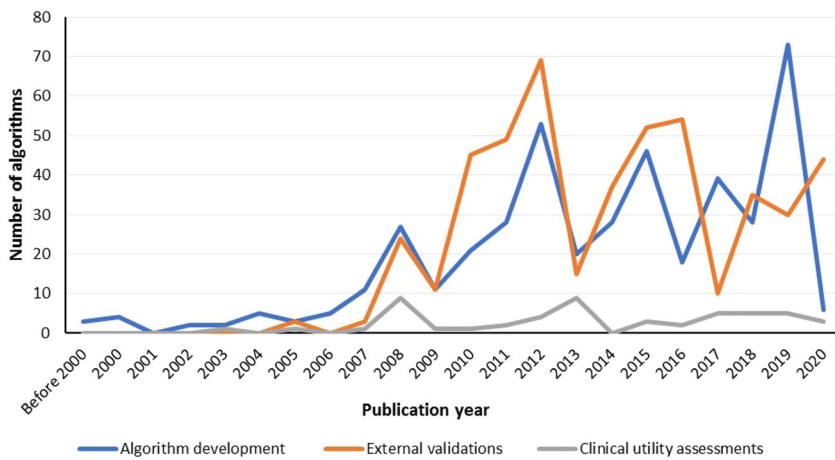


FIGURE 2 Algorithm development/evaluation by publication year

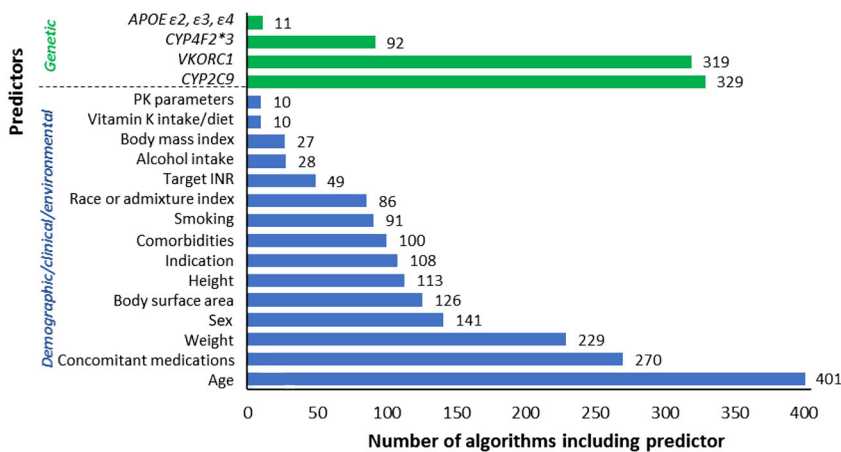


FIGURE 3 Predictors included in at least 10 algorithms. APOE, apolipoprotein E; CYP2C9, cytochrome P450, family 2, subfamily C, polypeptide 9; CYP4F2, cytochrome P450, family 4, subfamily F, polypeptide 2; PK parameters, pharmacokinetic parameters (S-warfarin clearance and/or distribution volume); INR, international normalized ratio; VKORC1, vitamin K epoxide reductase complex subunit 1

VKORC1-1639G > A (270 algorithms), VKORC1 1173C > T, (75 algorithms), VKORC1 3730G > A (20 algorithms) and a number of others (34 algorithms). Figure S3 shows numbers stratified by the 4 population categories. Age remained the most included demographic/clinical/environmental predictor in each of the 4 categories, while CYP2C9 remained the most common predictor in Whites, Blacks and the Mixed/Other population categories, but was overtaken by VKORC1 in Asians. The Asian algorithms that included the CYP2C9 gene ($n = 153$) mostly focused on the CYP2C9*3 variant ($n = 149$, 97%) as opposed to the CYP2C9*2 ($n = 44$, 29%) or other CYP2C9 ($n = 7$, 5%) variants. The corresponding proportions for inclusion of CYP2C9*3 vs CYP2C9*2 vs other CYP2C9 variants, respectively, were 99 vs 92 vs 19% (Whites, $n = 153$ algorithms), 99 vs 96 vs 36% (Blacks, $n = 99$) and 88 vs 95 vs 30% (Mixed/Other, $n = 64$).

3.3 | Predictive performance

A fit accuracy measure (the coefficient of determination, R^2) was the most commonly reported performance measure during both algorithm development (323 [75% of 433]) and external validation (261 [54% of 481]; Table 2). The R^2 value represents the proportion of total interpatient variability in warfarin dose requirements that can be jointly accounted for by the variables included in an algorithm. For

algorithm development, the median variability in warfarin dose explained by included predictors was 43% (range 2–96%). This was higher (median 45%, range 8–96%) when only pharmacogenetic algorithms were considered and lower (median 20%, range 2–83%) when only clinical factors were considered. The CYP2C9 and VKORC1 genes, respectively, accounted for a median of 7% (<1–50%) and median of 25% (1–59%) of the variability in warfarin dose requirements. The R^2 performance stratified by race is shown in Table S17.

A consideration of the race-specific proportions in each stratified analysis (Tables S10–S13) should be made when interpreting the race-stratified performances. For example, for 24 studies that included at least 5% Black patients, the proportion of warfarin dose variability that can be attributed to VKORC1 is 23%. However, these 24 studies on average included a median of only 13% (range 5–100%) Black patients. When only the 3 studies that included only Black patients are considered, the median VKORC1 partial R^2 becomes 9% (range 7–10%). These partial R^2 values should also be cautiously interpreted since different computation approaches yield different results (Figure S1).

Regarding the precision (predictive accuracy) and bias measures, the most reported measures were the mean absolute and mean prediction errors, respectively, being reported 137 (32%) and 17 (4%) times (algorithm development) and 222 (46%) and 144 (31%) times (external validations). The median mean absolute errors for the algorithm development and external validations were respectively

TABLE 2 Performance measures

Measures		Algorithm development (n = 433)		External validations (n = 481)	
		N ^a	Median (range)	N ^a	Median (range)
Fit accuracy	R ^{2b} (%)				
	All	323	43 (2–96 ^c)	261	39 (<1–86)
	Pharmacogenetic	273	45 (8–96)	232	41 (<1–86)
	Clinical ^d	178	20 (2–83)	29	24 (<1–69)
	CYP2C9	98	7 (<1–50)	-	-
	VKORC1	114	25 (1–59)	-	-
	Correlation coefficient				
	All	19	0.65 (0.31–0.82)	101	0.60 (0.03–0.86)
	Pharmacogenetic	15	0.65 (0.52–0.79)	97	0.60 (0.03–0.86)
	Clinical	4	0.56 (0.31–0.82)	4	0.32 (0.07–0.54)
Precision/predictive accuracy	Mean absolute error (mg/d) ^{e,f}				
	All	137	1.23 (0.11–2.89)	222	1.20 (0.37–3.70)
	Pharmacogenetic	105	1.26 (0.11–1.96)	185	1.18 (0.57–3.30)
	Clinical	32	1.10 (0.21–2.89)	37	1.34 (0.37–3.70)
	Mean square error (mg ² /d ²)				
	All	54	0.02 (0.01–0.74)	4	0.67 (0.60–0.74)
	Pharmacogenetic	30	0.02 (0.01–0.10)	-	-
	Clinical	24	0.02 (0.01–0.74)	4	0.67 (0.60–0.74)
	Root mean square error (mg/d)				
	All	14	0.80 (0.10–3.09)	68	1.44 (0.19–4.29)
	Pharmacogenetic	6	0.34 (0.10–1.44)	58	1.37 (0.19–4.29)
	Clinical	8	1.87 (0.66–3.09)	10	1.77 (0.66–2.33)
	Mean absolute percentage error (%) ^f				
	All	7	21 (13–54)	37	32 (20–53)
	Pharmacogenetic	6	25 (18–54)	34	32 (21–53)
	Clinical	1	19 (13–21)	3	34 (20–36)
	Unbiased mean absolute percentage Error (%)				
	All (clinical)	1	34	3	37 (36–38)
	Root mean square percentage error (%)				
	All (pharmacogenetic)	1	42	5	53 (37–99)
Bias	Mean prediction error (mg/d) ^f				
	All	17	0.01 (–0.28–0.60)	144	–0.20 (–3.94–1.80)
	Pharmacogenetic	9	–0.10 (–0.28–0.48)	140	–0.20 (–3.94–1.80)
	Clinical	8	0.04 (0.01–0.60)	4	–0.59 (–1.01–0.27)
	Mean percentage prediction error (%) ^f				
	All (pharmacogenetic)	3	4 (3–6)	26	22 (2–76)
	Logarithm of the accuracy ratio-derived (%)				
	All (clinical)	1	<1	3	8 (4–13)
Clinical relevance	Patients with predicted dose within 20% of actual (%)				
	All	132	48 (10–98)	245	43 (0–80)
	Pharmacogenetic	95	50 (30–98)	231	42 (0–80)

(Continues)

TABLE 2 (Continued)

Measures		Algorithm development (n = 433)		External validations (n = 481)	
		N ^a	Median (range)	N ^a	Median (range)
	Clinical	37	47 (10–87)	14	48 (26–63)
	Patients with predicted dose within 1 mg/d of actual (%)				
	All	14	63 (34–92)	47	42 (17–83)
	Pharmacogenetic	12	63 (34–92)	34	42 (17–83)
	Clinical	2	62 (36–87)	13	42 (22–70)

^aN represents the number of algorithms for which the respective measures were explored and reported. For algorithm development, both development and internal validation cohorts were included, if both reported, although the algorithm was still counted as 1. Results in figures were included if a numerical value was extractable.

^bAlso called the coefficient of determination. For the development cohort, adjusted values used, when reported.

^cThe highest R^2 reported in Pavani²⁹ as 94%/96%.

^dFrom clinical algorithms. For algorithm development, this also includes pharmacogenetic algorithms that reported R^2 contributions of clinical factors only.

^eIncludes 9 studies reporting median absolute error.

^fIn some studies (e.g. Botton,³⁰ You,³¹ Tan,³² Biss,³³ Zhou,³⁴ Lin,³⁵ Xie³⁶) these performance measures were unclear or inconsistent with their definitions (if available) and/or reported values, in which case a best guess was made. For example, a negative mean absolute error was likely to be a mean prediction error.

1.23 and 1.20 mg/d, with Asians (0.70 and 0.96 mg/d) and Whites (1.29 and 1.30 mg/d) having lower values when compared to Blacks (1.55 and 1.39 mg/d). The preferred precision and bias measures (Table S4) were underreported, each being reported only once and thrice for algorithm development and external validation, respectively. Clinical relevance and other fit accuracy, precision and bias measures are detailed in Tables 2 and S17.

Because most studies reported R^2 (a fit accuracy measure), we carried out a *posthoc* correlation analysis and included the studies that reported both the R^2 and a precision accuracy measure to determine whether R^2 could be a good proxy of predictive accuracy. For this purpose, we used the mean absolute error as the predictive accuracy measure because it was the most reported (its limitations as a predictive accuracy measure (Table S4) notwithstanding). A total of 216 algorithm developments and external validations reported both these 2 measures, with lower mean absolute errors being moderately associated with higher R^2 values (Pearson's product-moment correlation coefficient -0.390 [95% confidence intervals -0.494 to -0.274], Figure S4).

Tables 2 and S17 include the performance measures stratified according to whether algorithms were clinical or pharmacogenetic (direct comparisons are available for some algorithm pairs in Tables S5 and S7). To directly compare the performances of algorithms stratified according to the modelling technique and time of application (dose initiation or dose revision), we summarized the studies that, using the same dataset, included at least 2 algorithms that differed in these 2 characteristics. As expected, dose revision algorithms generally performed better than dose initiation algorithms (Table S18). Multiple linear regression performed comparable to or even better than many other machine learning techniques (Table S19). Although pharmacokinetic/pharmacodynamic algorithms (fitted using nonlinear mixed effect modelling) performed better than other algorithms, this is mainly attributable to their dose revision aspects (i.e. when used for

dose initiation, performance was comparable). However, the numbers of direct comparisons were few, and the performance metrics used were probably suboptimal (Table S4).

3.4 | Risk of bias

We focused on the assessment of the risk of bias in the analysis domain (Tables S3, S4, S6, S7 and S20). During algorithm development, most developments had the number of participants per candidate predictor variable ≥ 20 ($n = 203$, 47%), did not provide information on the handling of continuous and categorical predictors ($n = 291$, 67%), probably included all enrolled participants in the analysis ($n = 229$, 53%) and did not provide information on the handling of participants with missing data ($n = 233$, 54%; Table S20). Additionally, many algorithm developments relied on univariable ($n = 204$, 47%) and multivariable ($n = 208$, 48%) analysis during predictor selection, did not appropriately evaluate algorithm performance ($n = 232$, 54%), did not account for model overfitting and optimism in algorithm performance ($n = 300$, 69%), and did not provide enough information to assess whether predictors and their assigned weights in the final algorithms corresponded to the results reported in the multivariable analysis ($n = 220$, 51%). Consequently, only 1 (<1%) algorithm was rated as having a low risk of bias (unclear $n = 26$, 6%; high $n = 406$, 94%).

By contrast, most external validations included at least 100 participants with stable dose ($n = 329$, 68%), all probably appropriately handled continuous and categorical predictors ($n = 481$, 100%), mostly analysed all enrolled participants ($n = 309$, 64%) although many did not provide enough information on the handling of participants with missing data ($n = 293$, 61%). Most ($n = 273$, 57%) reported the precision measures we considered appropriate for this review, although only 8 (<2%) were rated as having a low risk of bias (unclear $n = 97$, 20%; high $n = 376$, 78%).

Although we did not focus on the risk of bias in the participant, predictors and outcome domains, the key risk of bias concerns in these domains are reported in Tables S6 (algorithm development) and S7 (external validation). Of note, despite large variability, most algorithm developments ($n = 386$, 89%) and external validations ($n = 433$, 90%) provided stable dose definitions and/or referenced previous publications in which the same were provided. Lastly, for algorithm development, we also explored whether the outcome of stable dose was transformed during analysis since outcome transformation may affect the bias of the algorithm (Asiimwe, unpublished data). Most algorithm developments ($n = 228$, 53%) did not incorporate any form of transformation, while 102 (24%) and 85 (20%) algorithm developments, respectively, incorporated logarithmic and square root transformations for reasons detailed in Table S21 (for 18 [4%] algorithms, information was not available). The most common reason provided was to normalize dose and limit heteroscedasticity ($n = 120$, 64%) with only 3 (2%) studies reporting clinical considerations as justification.

4 | DISCUSSION

To facilitate a literature search of warfarin dosing algorithms by clinicians, guideline developers and/or policymakers, we have provided a comprehensive summary of existing algorithms ($n = 433$), external validations ($n = 481$) and clinical utility assessments ($n = 52$) as well as described the populations for which they were developed. Using a threshold of at least 5% inclusion in a dataset, most algorithms were developed in Asians (49% of developed algorithms) and Whites (43%). Whereas 28% of the development datasets included Blacks, this group was under-represented, the median percentage of Black participants in those datasets being only 14% (Asians and Whites, by contrast, comprised 100 and 90% [medians] of their corresponding algorithm development datasets). Similar trends were observed in the external validations and clinical utility assessments, with these results echoing previous reports of underrepresentation of minority groups.^{6,10} The IWPC²³ population categories were reported in the main results. As a result, Hispanic Caucasians were grouped with European Caucasians, sub-Saharan Blacks with African Americans, Indians with Han-Chinese, multiple sub-populations under Mixed/Other etc.—groupings that simplify results' presentation but may be inaccurate in the context of personalized medicine. We therefore included locations (countries) from where the trial populations were recruited to serve as proxies for these sub-populations, and further disparities were revealed. For example, despite 28% of the algorithm developments, 24% of the external validations and 31% of the clinical utility assessments including at least 5% Blacks, <1% algorithm developments, <1% external validations and none of the clinical utility assessments were conducted in sub-Saharan Africa, results that re-affirm our previous report that very few studies are conducted in Africa.³⁷

Nonstatistical methods including clinical reasoning and literature support are recommended when deciding which candidate predictors to omit, combine or include during multivariable modelling.¹² To make it easier for those developing new or updating existing algorithms, we

also summarised the clinical, demographic, environmental, and genetic factors that are commonly included in warfarin dosing algorithms. The 4 most common demographic/clinical/environmental predictors were age, concomitant medications such as amiodarone, weight and sex being included in 93, 62, 53 and 32% of the 433 algorithms, respectively. By contrast, CYP2C9, VKORC1, and CYP4F2 variants were respectively included in 95, 92 and 27% of the 346 pharmacogenetic algorithms. All these are well-established predictors whose mechanisms of action have been previously extensively reported.^{7,38} In line with the ethnicity-specific differences in minor allele frequencies of the various genetic variants, population-specific differences were observed. For instance, CYP2C9*2 is almost absent in some Asian populations³⁹ and it was included in only 29% of Asian algorithms that included the CYP2C9 gene ($n = 153$; compared to being included in 92% of 153 White algorithms, 96% of 99 Black algorithms and 95% of 64 Mixed/Other algorithms). Other CYP2C9 variants (such as *5, *6, *8 and *11) were mostly included in Black (36% of 99) and Mixed/Other (30% of 64) algorithms and less frequently in Asian (5% of 153) and White (19% of 153) algorithms. Despite a higher inclusion of these other CYP2C9 variants in studies employing at least 5% Blacks, 36% may still be a low figure given the importance of these African-specific variants.³⁷ When undertaking multivariable modelling, other population- and/or clinical setting-specific considerations such as availability and cost of predictors should also always be considered.¹²

Our third objective was to evaluate the performances of these algorithms. As reported previously,⁴⁰ the coefficient of determination (R^2) was the most common performance measure (reported in 75% of algorithm developments and 54% of external validations). Based on R^2 , the median contribution of clinical factors (20%) and VKORC1 (25%) was similar to previous estimates^{7,38} although CYP2C9's contribution (7%) was lower (previously estimated at 12³⁸ and 15%⁷). Among the first of 2 key cautions is, like for all the other performance measures, these summary estimates were descriptive in nature since we did not conduct a formal quantitative synthesis, which with the preferred measures (Table S4) and methods (such as individual participant data meta-analysis⁴¹) is possible. Because of the descriptive nature of the study, different algorithms using the same or overlapping datasets was also of little concern. The second cautionary warning is that R^2 is a fit accuracy and not a prediction accuracy measure, the former of which is of less relevance when evaluating the value of prediction algorithms.^{42–44} For example, fit accuracy measures will mostly focus on the correct relative ordering of the dose predictions while predictive accuracy measures will also require that these predictions be close to the doses actually required by the patients. During a *posthoc* correlation analysis aimed at determining if R^2 could be a good proxy of 1 of the predictive accuracy measures (the mean absolute error, MAE), a moderate correlation coefficient (−0.39) was observed, which further questions the use of fit-accuracy measures given that predictive accuracy measures are available. Among the predictive accuracy distance measures (Table S4), the MAE is preferred to the [root] mean squared error mainly because it is less sensitive to outliers⁴⁵—and this would be an additional reason to prioritize it over R^2 , which is also highly sensitive to outliers. For

example, the exclusion of only 1 outlier (<0.1% of 1010 participants) in the IWPC internal validation cohort improved the performance of the pharmacogenetic algorithm from an R^2 of 33 to 43%²³ while in Langley's study ($n = 75$), the R^2 increased from 9 to 31% when 2 outliers were excluded.⁴⁶ To reiterate and for the reasons above, all the reported R^2 values, especially those that approach 100%, should be interpreted cautiously. Despite the mean absolute error being preferable to the above-mentioned measures, it remains a distance measure whose limitations we detail in Table S4. In the same table, we describe an unbiased predictive accuracy ratio measure (derived from the logarithm of the ratio of the predicted dose to the actual dose^{43,47}), which we consider to be most appropriate. Unfortunately, and excluding our own study (Asiimwe, unpublished data), this measure was not used. We conducted some comparisons in performance based on populations, modelling techniques and the time an algorithm is applied but these results should again be cautiously interpreted because few studies reported direct comparisons and the performance measures used were likely to be inappropriate. For example, it may be misleading to conclude that Asians are better dosed compared to Whites or Blacks based on mean absolute error (or any distance measure that ignores the actual dose required by a patient) since as explained in Table S4, an MAE of 1 mg/d in a small value (e.g. 2 mg/d) may be clinically more important than a larger error (e.g. 2 mg/d) in an even larger value (e.g. 5 mg/d). With these precautions in mind, multiple linear regression (the most commonly used technique) seemed to perform comparable or even better than other supervised machine learning techniques as previously observed.²³ A further understanding of these other techniques, and a more thorough comparison with multiple linear regression, is nevertheless recommended. For instance, artificial neural networks can capture very complex relationships,⁴⁸ while pharmacokinetic/pharmacodynamic-based techniques model both temporal and quantitative aspects of warfarin response and do not exclude unstable patients,⁴⁰ which may be beneficial to warfarin dosing.

Lastly, we assessed the risk of bias of existing algorithms with focus on the analysis domain. Less than 2% of both algorithm developments and external validations had a low risk of bias. Only our study was ranked as having a low risk of bias during algorithm development and although this could be because of self-evaluation, we mainly attribute it to following the TRIPOD (Transparent Reporting of a multivariable prediction model for Individual Prognosis Or Diagnosis) guidelines,⁴⁹ which if followed correctly would result in a low risk of bias rating with the risk of bias assessment tool that we used. It is of concern that although the TRIPOD guidelines were published in 2015, none of the other 163 studies reported from 2016 onwards refer to its use. In the context of not adhering to current methodological recommendations, warfarin dosing algorithms may not be unique.^{50,51} The consequences of most of the design flaws have been previously described in detail.⁵² One key issue that has received less attention is data transformation (done in 44% of the algorithm developments). As discussed by Keene,⁵³ we also discourage data-driven decisions to transform or not and recommend that the logarithmic transformation be preferred because it produces a proportional/multiplicative scale that is clinically relevant and easy to interpret.^{53,54} A slightly more

complex method to fit nontransformed dose using a proportional/multiplicative scale is to estimate the parameters of a linear algorithm using nonlinear (log-log) modelling^{43,47} as we previously did (Asiimwe, unpublished data).

In agreement with the CPIC guidelines,¹ we recommend the IWPC²³ and Gage¹⁴ clinical and pharmacogenetic algorithms since these have been the most externally validated and clinically assessed algorithms. Specifically, clinical utility assessments have concluded that they are better than fixed dose-initiation approaches.^{15–22} Recent debate has mainly focused on whether pharmacogenetic-guided dosing strategies are better than clinical-guided strategies with randomized controlled trials such as Kimmel *et al.*,⁵⁵ Pirmohamed *et al.*⁵⁶ and Gage *et al.*⁵⁷ providing conflicting results—we neither quantitatively synthesized (both benefit and safety) nor assessed the risk of bias of the clinical utility studies since we felt these have been previously explored in more detail in several systematic reviews and meta-analyses.^{15–22}

In addition to the CPIC guidance, before using these or other algorithms, clinicians, guideline developers and/or policymakers are reminded to ensure their applicability to their respective populations. For example, the above pharmacogenetic algorithms, despite including Black patients, may not be appropriate for Blacks because they exclude important Black-specific genetic variants. Clinicians are also reminded that other numerous dosing algorithms that were not assessed in this review exist and may be more appropriate depending on the clinical setting. For example, we excluded many algorithms that rely only on current dose and measured INR levels to make this review more manageable, while the Food and Drug Administration dosing table was excluded because the methods used to derive this table are not publicly available. Nevertheless, these algorithms are less likely to perform better than those that incorporate predictors additional to existing dose/measured INR while the Food and Drug Administration table has been assessed in several studies^{58–64} and its performance is not better than the pharmacogenetic algorithms we have reported here.

In addition to using heterogeneous and nonspecific racial categories, presenting mainly descriptive results, and excluding algorithms that rely only on current dose and measured INR levels, our study had other limitations. Specifically, we did not include non-English articles, which could have affected geographical representation. For example, we excluded 9 Chinese studies during title/abstract screening and non-English articles are less likely to be indexed in MEDLINE.⁶⁵ Although we tried identifying other studies through reference list searching, using only the MEDLINE database also limited the number of studies that we could include in this review. Lastly, we relied on single-reviewer extraction; a second reviewer, nevertheless, confirmed consistency based on a random selection of 10% of the included papers.

For further research, novel/existing algorithms may need to be developed or updated and externally validated following the recommended guidelines such as TRIPOD.⁴⁹ More attention needs to be paid to under-represented populations such as minority ethnic groups and children (only 3% developed algorithms) to reduce health disparities. Moreover, although newer directly acting oral anticoagulants have been developed, warfarin is likely to remain the preferred choice for some of these groups.⁶⁶

In conclusion, this systematic review provides a comprehensive summary of the algorithms available for different populations and their associated covariates (demographic, clinical, environmental and/or genetic), performances and risk of bias from these algorithms. Most of these algorithms have been developed for Asians and Whites, most have neither been externally validated nor assessed for clinical utility and either have a high or unclear risk of bias, which makes their reliability for clinical use uncertain. Future research should focus on developing prediction algorithms for under-represented populations and externally validating and assessing the clinical utility of these and already existing algorithms. Algorithm development and assessment should follow current methodological recommendations to improve reliability and applicability.

ACKNOWLEDGEMENTS

I.G.A. thanks the University of Liverpool for studentship funding support. This research was commissioned by the National Institute for Health Research (NIHR) Global Health Research Group on Warfarin anticoagulation in patients with cardiovascular disease in sub-Saharan Africa [ref: 16/137/101] using UK aid from the UK Government. The views expressed in this publication are those of the author(s) and not necessarily those of the NIHR or the Department of Health and Social Care. We also thank the MRC Centre for Drug Safety Science for infrastructure support. M.P. is Emeritus NIHR Senior Investigator.

COMPETING INTERESTS

M.P. receives other research funding from various organisations including the EU Commission. He has also received partnership funding for the following: MRC Clinical Pharmacology Training Scheme (co-funded by MRC and Roche, UCB, Eli Lilly and Novartis); a PhD studentship jointly funded by EPSRC and Astra Zeneca; and grant funding from Vistagen Therapeutics. He has also unrestricted educational grant support for the UK Pharmacogenetics and Stratified Medicine Network from Bristol-Myers Squibb and UCB. He has developed an HLA genotyping panel with MC Diagnostics, but does not benefit financially from this. None of these of additional funding sources have been used for the current paper.

CONTRIBUTORS

I.G.A., E.J.Z., A.L.J. and M.P. conceived and designed the study. I.G.A. and R.O. performed data search, screening and analysis. A.L.J. and M.P. supervised the study. I.G.A. wrote the manuscript. A.L.J. and M.P. interpreted the results and made manuscript revisions. All authors read and approved the final manuscript.

DATA AVAILABILITY STATEMENT

All relevant material is provided in the supplementary material.

ORCID

Innocent G. Asiimwe  <https://orcid.org/0000-0002-1196-1822>

Munir Pirmohamed  <https://orcid.org/0000-0002-7534-7266>

REFERENCES

- Johnson JA, Caudle KE, Gong L, et al. Clinical Pharmacogenetics implementation consortium (CPIC) guideline for Pharmacogenetics-guided warfarin dosing: 2017 update. *Clin Pharmacol Ther.* 2017; 102(3):397-404.
- Finkelman BS, French B, Bershaw L, et al. Predicting prolonged dose titration in patients starting warfarin. *Pharmacoepidemiol Drug Saf.* 2016;25(11):1228-1235.
- Lee MT, Klein TE. Pharmacogenetics of warfarin: challenges and opportunities. *J Hum Genet.* 2013;58(6):334-338.
- Turner RM, Pirmohamed M. Cardiovascular pharmacogenomics: expectations and practical benefits. *Clin Pharmacol Ther.* 2014;95(3): 281-293.
- Sharabiani A, Nutescu EA, Galanter WL, Darabi H. A new approach towards minimizing the risk of Misdosing warfarin initiation doses. *Comput Math Methods Med.* 2018;2018:1-11, 5340845.
- Cavallari LH, Perera MA. The future of warfarin pharmacogenetics in under-represented minority groups. *Future Cardiol.* 2012;8(4): 563-576.
- Pirmohamed M, Kamali F, Daly AK, Wadelius M. Oral anticoagulation: a critique of recent advances and controversies. *Trends Pharmacol Sci.* 2015;36(3):153-163.
- Saffian SM, Duffull SB, Wright D. Warfarin dosing algorithms Underpredict dose requirements in patients requiring ≥ 7 mg daily: a systematic review and meta-analysis. *Clin Pharmacol Ther.* 2017;102 (2):297-304.
- Verhoef TI, Redekop WK, Daly AK, van Schie RM, de Boer A, Maitland-van der zee AH. Pharmacogenetic-guided dosing of coumarin anticoagulants: algorithms for warfarin, acenocoumarol and phenprocoumon. *Br J Clin Pharmacol.* 2014;77(4):626-641.
- Shendre A, Dillon C, Limdi NA. Pharmacogenetics of warfarin dosing in patients of African and European ancestry. *Pharmacogenomics.* 2018;19(17):1357-1371.
- Moons KG, de Groot JA, Bouwmeester W, et al. Critical appraisal and data extraction for systematic reviews of prediction modelling studies: the CHARMS checklist. *PLoS Med.* 2014;11(10):1-12, e1001744.
- Wolff RF, Moons KGM, Riley RD, et al. PROBAST: a tool to assess the risk of bias and applicability of prediction model studies. *Ann Intern Med.* 2019;170(1):51-58.
- Grosse SD, Khoury MJ. What is the clinical utility of genetic testing? *Genet Med.* 2006;8(7):448-450.
- Gage BF, Eby C, Johnson JA, et al. Use of pharmacogenetic and clinical factors to predict the therapeutic dose of warfarin. *Clin Pharmacol Ther.* 2008;84(3):326-331.
- Franchini M, Mengoli C, Cruciani M, Bonfanti C, Mannucci PM. Effects on bleeding complications of pharmacogenetic testing for initial dosing of vitamin K antagonists: a systematic review and meta-analysis. *J Thromb Haemost.* 2014;12(9):1480-1487.
- Stergiopoulos K, Brown DL. Genotype-guided vs clinical dosing of warfarin and its analogues: meta-analysis of randomized clinical trials. *JAMA Intern Med.* 2014;174(8):1330-1338.
- Tang Q, Zou H, Guo C, Liu Z. Outcomes of pharmacogenetics-guided dosing of warfarin: a systematic review and meta-analysis. *Int J Cardiol.* 2014;175(3):587-591.
- Liao Z, Feng S, Ling P, Zhang G. Meta-analysis of randomized controlled trials reveals an improved clinical outcome of using genotype plus clinical algorithm for warfarin dosing. *J Thromb Thrombolysis.* 2015;39(2):228-234.
- Tang T, Liu J, Zuo K, et al. Genotype-guided dosing of Coumarin anticoagulants: a meta-analysis of randomized controlled trials. *J Cardiovasc Pharmacol Ther.* 2015;20(4):387-394.
- Shi C, Yan W, Wang G, Wang F, Li Q, Lin N. Pharmacogenetics-based versus conventional dosing of warfarin: a meta-analysis of

- randomized controlled trials. *PLoS ONE*. 2015;10(12):1-16, e0144511.
21. Tse G, Gong M, Li G, et al. Genotype-guided warfarin dosing vs. conventional dosing strategies: a systematic review and meta-analysis of randomized controlled trials. *Br J Clin Pharmacol*. 2018; 84(9):1868-1882.
 22. Yang T, Zhou Y, Chen C, Lu M, Ma L, Cui Y. Genotype-guided dosing versus conventional dosing of warfarin: a meta-analysis of 15 randomized controlled trials. *J Clin Pharm Ther*. 2019;44(2): 197-208.
 23. International Warfarin Pharmacogenetics Consortium, Klein TE, Altman RB, et al. Estimation of the warfarin dose with clinical and pharmacogenetic data. *N Engl J Med*. 2009;360(8):753-764.
 24. R: A language and environment for statistical computing [computer program]. Vienna: R Foundation for Statistical Computing; 2019.
 25. Sconce EA, Khan TI, Wynne HA, et al. The impact of CYP2C9 and VKORC1 genetic polymorphism and patient characteristics upon warfarin dose requirements: proposal for a new dosing regimen. *Blood*. 2005;106(7):2329-2333.
 26. Wadelius M, Chen LY, Lindh JD, et al. The largest prospective warfarin-treated cohort supports genetic forecasting. *Blood*. 2009; 113(4):784-792.
 27. Huang SW, Chen HS, Wang XQ, et al. Validation of VKORC1 and CYP2C9 genotypes on interindividual warfarin maintenance dose: a prospective study in Chinese patients. *Pharmacogenet Genomics*. 2009;19(3):226-234.
 28. Lenzini P, Wadelius M, Kimmel S, et al. Integration of genetic, clinical, and INR data to refine warfarin dosing. *Clin Pharmacol Ther*. 2010;87 (5):572-578.
 29. Pavani A, Naushad SM, Kumar RM, Srinath M, Malempati AR, Kutala VK. Artificial neural network-based pharmacogenomic algorithm for warfarin dose optimization. *Pharmacogenomics*. 2016;17 (2):121-131.
 30. Botton MR, Bandinelli E, Rohde LE, Amon LC, Hutz MH. Influence of genetic, biological and pharmacological factors on warfarin dose in a southern Brazilian population of European ancestry. *Br J Clin Pharmacol*. 2011;72(3):442-450.
 31. You JH, Wong RS, Waye MM, et al. Warfarin dosing algorithm using clinical, demographic and pharmacogenetic data from Chinese patients. *J Thromb Thrombolysis*. 2011;31(1):113-118.
 32. Tan SL, Li Z, Song GB, et al. Development and comparison of a new personalized warfarin stable dose prediction algorithm in Chinese patients undergoing heart valve replacement. *Pharmazie*. 2012;67 (11):930-937.
 33. Biss TT, Avery PJ, Brandao LR, et al. VKORC1 and CYP2C9 genotype and patient characteristics explain a large proportion of the variability in warfarin dose requirement among children. *Blood*. 2012;119(3): 868-873.
 34. Zhou Q, Kwong J, Chen J, et al. Use of artificial neural network to predict warfarin individualized dosage regime in Chinese patients receiving low-intensity anticoagulation after heart valve replacement. *Int J Cardiol*. 2014;176(3):1462-1464.
 35. Lin M, Yu L, Qiu H, Wang Q, Zhang J, Song H. Verification of five pharmacogenomics-based warfarin administration models. *Indian J Pharm*. 2016;48(3):258-263.
 36. Xie C, Xue L, Zhang Y, et al. Comparison of the prediction performance of different warfarin dosing algorithms based on Chinese patients. *Pharmacogenomics*. 2020;21(1):23-32.
 37. Asiimwe IG, Zhang EJ, Osanlou R, et al. Genetic factors influencing warfarin dose in black-African patients: a systematic review and meta-analysis. *Clin Pharmacol Ther*. 2020;107(6): 1420-1433.
 38. Baker WL, Johnson SG. Pharmacogenetics and oral antithrombotic drugs. *Curr Opin Pharmacol*. 2016;27:38-42.
 39. Genomes Project C, Auton A, Brooks LD, et al. A global reference for human genetic variation. *Nature*. 2015;526(7571):68-74.
 40. Hamberg AK, Wadelius M. Pharmacogenetics-based warfarin dosing in children. *Pharmacogenomics*. 2014;15(3):361-374.
 41. Sutton AJ, Higgins JP. Recent developments in meta-analysis. *Stat Med*. 2008;27(5):625-650.
 42. Alexander DL, Tropsha A, Winkler DA. Beware of R(2): simple, unambiguous assessment of the prediction accuracy of QSAR and QSPR models. *J Chem Inf Model*. 2015;55(7):1316-1322.
 43. Lo B, Gao X. Assessing software cost estimation models: criteria for accuracy, consistency and regression. *Australas J Inf Syst*. 1997;5(1): 30-44.
 44. Sheiner LB, Beal SL. Some suggestions for measuring predictive performance. *J Pharmacokinet Biopharm*. 1981;9(4):503-512.
 45. Chai T, Draxler RR. Root mean square error (RMSE) or mean absolute error (MAE)? –arguments against avoiding RMSE in the literature. *Geosci Model Dev*. 2014;7:1247-1250.
 46. Langley MR, Booker JK, Evans JP, McLeod HL, Weck KE. Validation of clinical testing for warfarin sensitivity: comparison of CYP2C9-VKORC1 genotyping assays and warfarin-dosing algorithms. *J Mol Diagn*. 2009;11(3):216-225.
 47. Tofallis C. A better measure of relative prediction accuracy for model selection and model estimation. *J Oper Res Soc*. 2015;66(8): 1352-1362.
 48. Grossi E, Podda GM, Pugliano M, et al. Prediction of optimal warfarin maintenance dose using advanced artificial neural networks. *Pharmacogenomics*. 2014;15(1):29-37.
 49. Moons KG, Altman DG, Reitsma JB, et al. Transparent reporting of a multivariable prediction model for individual prognosis or diagnosis (TRIPOD): explanation and elaboration. *Ann Intern Med*. 2015;162(1): W1-W73.
 50. Bouwmeester W, Zuithoff NP, Mallett S, et al. Reporting and methods in clinical prediction research: a systematic review. *PLoS Med*. 2012;9(5):1-12.
 51. Mallett S, Royston P, Dutton S, Waters R, Altman DG. Reporting methods in studies developing prognostic models in cancer: a review. *BMC Med*. 2010;8(20):1-11.
 52. Moons KGM, Wolff RF, Riley RD, et al. PROBAST: a tool to assess risk of bias and applicability of prediction model studies: explanation and elaboration. *Ann Intern Med*. 2019;170(1):W1-W33.
 53. Keene ON. The log transformation is special. *Stat Med*. 1995;14(8): 811-819.
 54. Vittinghoff E, Glidden D, Shiboski S, McCulloch C. *Regression methods in biostatistics*. New York: Springer; 2012.
 55. Kimmel SE, French B, Kasner SE, et al. A pharmacogenetic versus a clinical algorithm for warfarin dosing. *N Engl J Med*. 2013;369(24): 2283-2293.
 56. Pirmohamed M, Burnside G, Eriksson N, et al. A randomized trial of genotype-guided dosing of warfarin. *N Engl J Med*. 2013;369(24): 2294-2303.
 57. Gage BF, Bass AR, Lin H, et al. Effect of genotype-guided warfarin dosing on clinical events and anticoagulation control among patients undergoing hip or knee arthroplasty: the GIFT randomized clinical trial. *JAMA*. 2017;318(12):1115-1124.
 58. Finkelman BS, Gage BF, Johnson JA, Brensinger CM, Kimmel SE. Genetic warfarin dosing: tables versus algorithms. *J Am Coll Cardiol*. 2011;57(5):612-618.
 59. Shin J, Cao D. Comparison of warfarin pharmacogenetic dosing algorithms in a racially diverse large cohort. *Pharmacogenomics*. 2011; 12(1):125-134.
 60. Bazan NS, Sabry NA, Rizk A, Mokhtar S, Badary O. Validation of pharmacogenetic algorithms and warfarin dosing table in Egyptian patients. *Int J Clin Pharmacol*. 2012;34(6):837-844.
 61. Ramirez AH, Shi Y, Schildcrout JS, et al. Predicting warfarin dosage in European-Americans and African-Americans using DNA samples

- linked to an electronic health record. *Pharmacogenomics*. 2012;13(4): 407-418.
62. Shahabi P, Scheinfeldt LB, Lynch DE, et al. An expanded pharmacogenomics warfarin dosing table with utility in generalised dosing guidance. *Thromb Haemost*. 2016;116(2):337-348.
63. Wiley LK, Vanhouten JP, Samuels DC, et al. Strategies for equitable Pharmacogenomic-guided warfarin dosing among European and African American individuals in a clinical population. *Pac Symp Biocomput*. 2017;22:545-556.
64. Selim TE, Azzam HA, Ghoneim HR, Mohamed AA, El Wakeel H, Abu Bakr HM. Pharmacogenetic warfarin dosing algorithms: validity in Egyptian patients. *Acta Haematol*. 2018;139(4):255-262.
65. Loria A, Arroyo P. Language and country preponderance trends in MEDLINE and its causes. *J Med Libr Assoc*. 2005;93(3): 381-385.
66. Pirmohamed M. Warfarin: the end or the end of one size fits all therapy? *J Pers Med*. 2018;8(22):1-9.

SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section at the end of this article.

How to cite this article: Asiimwe IG, Zhang EJ, Osanlou R, Jorgensen AL, Pirmohamed M. Warfarin dosing algorithms: A systematic review. *Br J Clin Pharmacol*. 2020;1–13. <https://doi.org/10.1111/bcp.14608>